

Rec'd PCT/PTO 20 AUG 2004



PCT

RAW SEQUENCE LISTING

DATE: 08/26/2004

PATENT APPLICATION: US/10/505,145

TIME: 11:31:53

Input Set : A:\56159-5241 Sequence Listing.txt

Output Set: N:\CRF4\08262004\J505145.raw

3 <110> APPLICANT: COLLIVER, Steven Peter
 4 DOBB, Roy Thomas
 5 van der HIJDEN, Hendrikus Theodorus Wilhelmus Maria
 7 <120> TITLE OF INVENTION: PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS
 9 <130> FILE REFERENCE: 56159-5241
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/505,145
 C--> 11 <141> CURRENT FILING DATE: 2004-08-20
 11 <150> PRIOR APPLICATION NUMBER: PCT/EP03/01465
 12 <151> PRIOR FILING DATE: 2003-02-13
 14 <150> PRIOR APPLICATION NUMBER: EP 02251404.6
 15 <151> PRIOR FILING DATE: 2002-02-28
 17 <160> NUMBER OF SEQ ID NOS: 59
 19 <170> SOFTWARE: PatentIn version 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 946
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Pisum sativum
 26 <400> SEQUENCE: 1
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 29 cctgttggtg gaatgggagc agcacctgac ttcacatgca agaaagacac taaagaagca 120
 31 atcatcgaag ccatcaaaca aggttacaga cactttgata ctgctgctgc ttatggatcc 180
 33 gaacaagctc ttggtgaggc tttgaatgag gctattcaac ttggtcttgt cactagagaa 240
 35 cagctttttg ttactttctaa actttgggtt actgaaaatc atcctcacct tgttcttcct 300
 37 gctctacaaa aatctctcaa gactcttcag ttggattact tggatttgta tttgattcat 360
 39 tggccactta gttctcagcc cggaaagttt tcatttccaa ttgatgtggc tgatctattg 420
 41 ccatttgatg taaaagggtg gtgggaatcc atggaagagg ctttgagact tggactcacg 480
 43 aaagctattg gtgtcagtaa cttctctgtc aagaaacttc aaaagctact atctgttgcc 540
 45 actgttcttc ctgctgttaa tcaagtagag atgaaccttg catggcaaca aaagaagcta 600
 47 agagaatttt gcaatgaaaa tggaaatagtg ttgactgcat tttcaccgtt gaggaaaggc 660
 49 gccagccgag gagcaaatga ggttatggag aatgatatgc ttaaacagat tgcagatgct 720
 51 catggaaagt ctattgcaca aatttctctg agatgggtat atgaacaagg aatcactttt 780
 53 gttccaaaga gctatgataa ggagagaatg agtcaaaatt tgagaatctt tgattggaca 840
 55 ctgacaaagg aggatcatga gaaaattgat caaattaagc agaatcgttt gatccctgga 900
 57 ccaaccaagc caagtctcaa tgatctttgg gatgatgaaa tataag 946
 60 <210> SEQ ID NO: 2
 61 <211> LENGTH: 314
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Pisum sativum
 65 <400> SEQUENCE: 2
 67 Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ala
 68 1 5 10 15
 71 Gln Ile Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
 72 20 25 30

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75 Cys Lys Lys Asp Thr Lys Glu Ala Ile Ile Glu Ala Ile Lys Gln Gly
76          35          40          45
79 Tyr Arg His Phe Asp Thr Ala Ala Tyr Gly Ser Glu Gln Ala Leu
80          50          55          60
83 Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
84 65          70          75          80
87 Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
88          85          90          95
91 Leu Val Leu Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp
92          100          105          110
95 Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
96          115          120          125
99 Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
100          130          135          140
103 Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
104 145          150          155          160
107 Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu
108          165          170          175
111 Leu Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
112          180          185          190
115 Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Glu Asn Gly
116          195          200          205
119 Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
120          210          215          220
123 Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
124 225          230          235          240
127 His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
128          245          250          255
131 Gly Ile Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln
132          260          265          270
135 Asn Leu Arg Ile Phe Asp Trp Thr Leu Thr Lys Glu Asp His Glu Lys
136          275          280          285
139 Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
140          290          295          300
143 Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
144 305          310
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 1567
149 <212> TYPE: DNA
150 <213> ORGANISM: Glycine max
152 <400> SEQUENCE: 3
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155 acaccactg caaaatcaaa agcacttcgc catctcccaa accaccaag cccaaagcct 120
157 cgtcttccct tcataggaca cttcatctc ttaaaagaca aacttctcca ctacgcactc 180
159 atcgacctct ccaaaaaaca tggtcctta ttctctctct actttggctc catgccaacc 240
161 gttgttgctt ccacaccaga attgttcaag ctcttctctc aaacgcacga ggcaacttcc 300
163 ttcaacacaa ggttccaaac ctcagccata agacgcctca cctatgatag ctcagtggca 360
165 atggttccct tcgggcccta ctggaagttc gtgaggaagc tcatcatgaa cgaccttctc 420
167 aacgccacca ctgtaaaca gttgaggcct ttgaggaccc aacagacgcg taagtctctt 480

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169 agggttatgg cccaaggcgc agaggcacag aagccccttg acttgaccga ggagcttctg 540
171 aaatggacca acagcaccat ctccatgatg atgctcggcg aggctgagga gatcagagac 600
173 atcgctcgcg aggttcttaa gatctttggc gaatacagcc tctactgactt catctggcca 660
175 ttgaagcatc tcaagggttg aaagtatgag aagaggatcg acgacatctt gaacaagttc 720
177 gaccctgtcg ttgaaagggg catcaagaag cgccgtgaga tcgtgaggag gagaaagaac 780
179 ggagaggttg ttgagggtga ggtcagcggg gttttccttg acactttgct cgagttcgct 840
181 gaggatgaga ctatggagat caaaatcacc aaggaccaca tcaagggtct tgttgtagac 900
183 tttttctcgg caggaacaga ctcaacagcg gtggcaacag agtgggcatt ggcagaactc 960
185 atcaacaatc ctaagggtgt ggaaaaggct cgtgaggagg tctacagtgt tgtgggaaag 1020
187 gacagacttg tggacgaagt tgacactcaa aaccttcctt acattagagc aatcgtgaag 1080
189 gagacattcc gcatgcaccc gccactccca gtggtcaaaa gaaagtgcac agaagagtgt 1140
191 gagattaatg gatatgtgat ccagagggga gcattgattc tcttcaatgt atggcaagta 1200
193 ggaagagacc ccaatactg ggacagacca tcggagttcc gtcttgagag gttcctagag 1260
195 acaggggctg aaggggaagc agggcctctt gatcttaggg gacaacattt tcaacttctc 1320
197 ccatttgggt ctgggaggag aatgtgccct ggagtcaatc tggctacttc gggaatggca 1380
199 acacttcttg catctcttat tcagtgtctt gacttgcaag tgctgggtcc acaaggacag 1440
201 atattgaagg gtggtgacgc caaagttagc atggaagaga gagccggcct cactgttcca 1500
203 agggcacata gtcttgtctg tgttcactt gcaaggatcg gcgttgcatc taaactcctt 1560
205 tcttaag

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208 <210> SEQ ID NO: 4

209 <211> LENGTH: 521

210 <212> TYPE: PRT

211 <213> ORGANISM: Glycine max

213 <400> SEQUENCE: 4

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215 Met Val Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
216 1 5 10 15
219 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
220 20 25 30
223 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
224 35 40 45
227 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
228 50 55 60
231 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
232 65 70 75 80
235 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
236 85 90 95
239 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
240 100 105 110
243 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
244 115 120 125
247 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
248 130 135 140
251 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
252 145 150 155 160
255 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
256 165 170 175
259 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
260 180 185 190
263 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile

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264          195          200          205
267 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
268          210          215          220
271 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
272 225          230          235          240
275 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
276          245          250          255
279 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
280          260          265          270
283 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
284          275          280          285
287 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
288          290          295          300
291 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
292 305          310          315          320
295 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
296          325          330          335
299 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
300          340          345          350
303 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
304          355          360          365
307 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
308          370          375          380
311 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
312 385          390          395          400
315 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
316          405          410          415
319 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
320          420          425          430
323 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
324          435          440          445
327 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
328          450          455          460
331 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
332 465          470          475          480
335 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
336          485          490          495
339 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
340          500          505          510
343 Ile Gly Val Ala Ser Lys Leu Leu Ser
344          515          520
347 <210> SEQ ID NO: 5
348 <211> LENGTH: 670
349 <212> TYPE: DNA
350 <213> ORGANISM: Lotus corniculatus
352 <400> SEQUENCE: 5
353 atggctgcat ccctcacccc aatccagggtc gagaaccttc aatttcctgc gtctgtcacc 60
355 tctccagcca cgcceaagtc ttatttcctc ggtggtgcag gggagagagg gttgacgatt 120
357 gaggggaagt tcataaaatt cactggcata ggagtgtatt tggaagatac agcagtggat 180

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359 tcaactcgcca ccaagtggaa gggtaagagt tcacaagagc tgcaggactc ccttgacttc 240
361 ttcagagaca tcatttcaag tccctctgag aagttaattc gaggggtccaa gctgaggcca 300
363 ttgagtggcg tggagtattc aagaaagggtg atggagaatt gtgtggcaca catgaagtct 360
365 gctggaactt atggtgaagc agaggccaca gccattgaaa aatttgcaga agccttcagg 420
367 aaggtggatt ttccaccagg ttcctctgtt ttctaccgac aatcaacaga tggaaaatta 480
369 gggcttagtt tctctttgga tgacacgata ccagaagaag aggctgtagt tatagagaac 540
371 aaggcactct cagaggcagt gttagagacc atgattggcg agcatgctgt ttcccctgat 600
373 ttgaagcggt gtttggctga aaggttgccct attgtgatga accaggggtct tctcctcact 660
375 ggaaactgat 670

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378 <210> SEQ ID NO: 6

379 <211> LENGTH: 222

380 <212> TYPE: PRT

381 <213> ORGANISM: Lotus corniculatus

383 <400> SEQUENCE: 6

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385 Met Ala Ala Ser Leu Thr Pro Ile Gln Val Glu Asn Leu Gln Phe Pro
386 1 5 10 15
389 Ala Ser Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly
390 20 25 30
393 Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr
394 35 40 45
397 Gly Ile Gly Val Tyr Leu Glu Asp Thr Ala Val Asp Ser Leu Ala Thr
398 50 55 60
401 Lys Trp Lys Gly Lys Ser Ser Gln Glu Leu Gln Asp Ser Leu Asp Phe
402 65 70 75 80
405 Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu Lys Leu Ile Arg Gly Ser
406 85 90 95
409 Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg Lys Val Met Glu
410 100 105 110
413 Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu Ala Glu
414 115 120 125
417 Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
418 130 135 140
421 Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu
422 145 150 155 160
425 Gly Leu Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val
426 165 170 175
429 Val Ile Glu Asn Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile
430 180 185 190
433 Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg
434 195 200 205
437 Leu Pro Ile Val Met Asn Gln Gly Leu Leu Leu Thr Gly Asn
438 210 215 220

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441 <210> SEQ ID NO: 7

442 <211> LENGTH: 9

443 <212> TYPE: PRT

444 <213> ORGANISM: Artificial Sequence

446 <220> FEATURE:

447 <223> OTHER INFORMATION: Description of Artificial Sequence: conserved

448 regions of various known CHR's

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date